## IN THE SPECIFICATION:

Please replace Paragraph No. 00055 with the following paragraph:

The present invention provides purified and isolated polynucleotides (*e.g.*, DNA sequences and RNA transcripts, both sense and complementary antisense strands, both single- and double-stranded, including splice variants thereof) that encode unknown G protein-coupled receptors heretofore termed novel GPCRs, or nGPCRs. Table 1 below identifies the SEQ ID NO: of the gene sequence, the SEQ ID NO: of the polypeptide encoded thereby, and the U.S. Provisional Application in which the gene sequence has been disclosed.

Table 1

nGPCR	Nucleotide	Amino acid	Originally filed in:
	Sequence (SEQ ID NO:)	Sequence (SEQ ID NO:)	
2037	1	2, 3	A, B

## Legend

A = Ser. No. 60/195,228

B = Ser. No. 60/251,313

Please replace Paragraph No. 00117 with the following paragraph:

Variant polypeptides include those wherein conservative substitutions have been introduced by modification of polynucleotides encoding polypeptides of the invention. Amino acids can be classified according to physical properties and contribution to secondary and tertiary protein structure. A conservative substitution is recognized in the art as a substitution of one amino acid for another amino acid that has similar properties. Exemplary conservative substitutions are set out in Table 2 (from WO 97/09433, page 10, published March 13, 1997 (PCT/GB96/02197, filed 9/6/96), immediately below.

Table 2

Conservative Substitutions I

SIDE CHAIN

CHARACTERISTIC	AMINO ACID
Aliphatic	
Non-polar	GAP
	$1/1$ $\sim$
Polar - uncharged	СЅТМ
	NQ
Polar - charged	D E
	KR
Aromatic	HFWY
Other	N Q D E

Please replace Paragraph No. 00118 with the following paragraph:

Alternatively, conservative amino acids can be grouped as described in Lehninger, (*Biochemistry*, Second Edition; Worth Publishers, Inc. NY, NY (1975), pp.71-77) as set out in Table 3, below.

Table 3

Conservative Substitutions II

## SIDE CHAIN

<u>CHARACTERISTIC</u>	AMINO ACID
Non-polar (hydrophobic)	_
A. Aliphatic:	ALIVP
B. Aromatic:	F W
C. Sulfur-containing:	M
D. Borderline:	G
Uncharged-polar	
A. Hydroxyl:	STY
B. Amides:	N Q
C. Sulfhydryl:	(,
D. Borderline:	G
Positively Charged (Basic):	KRH
Negatively Charged (Acidic):	DE

Please replace Paragraph No. 00119 with the following paragraph:

-- As still another alternative, exemplary conservative substitutions are set out in Table 4, below.

Table 4
Conservative Substitutions III

Original Residue	Exemplary Substitution
Ala (A)	Val, Leu, Ile
Arg (R)	Lys, Gln. Asn
Asn (N)	Gln, His, Lys, Arg
Asp (D)	Glu
Cys (C)	Ser
Gln (Q)	Asn
Glu (E)	Asp
His (H)	Asn, Gln, Lys, Arg
Ile (I)	Leu, Val, Met, Ala, Phe.
Leu (L)	Ile, Val, Met, Ala, Phe
Lys (K)	Arg, Gln, Asn

Met (M)	Leu, Phe, He
Phe (F)	Leu, Val, Ile, Ala
Pro (P)	Gly
Ser (S)	Thr
Thr (T)	Ser
Trp (W)	Туг
Tyr (Y)	Trp, Phe, Thr, Ser
Val (V)	Ile, Leu, Met, Phe, Ala

Please replace Paragraph No. 00236 with the following paragraph:

The following Table 5 contains the sequences of the polynucleotides and polypeptides of the invention. The transmembrane domains within the polypeptide sequence are identified by underlining.

Table 5			
The following DNA sequence nGPCR-2037 <seq 1="" id="" no.=""> was identified in 11. sapiens:</seq>			
THE TARGETT OF THE	GAATOTAACTTOTGTALUWA (TIGTSAA		
#A - T - ATGCT BROAGCTCT BOTTT BOAGACTCT AACT			
**** "AMETTGAAGGAAGGTACCTGCCCTCTGATT(	CCAGGACTGGAGAACUATCALCCCGGCT		
ATTENT THAT GRATATOTACCTGGTGGGCTTCGTGGG			
ACAATOOTTGSAAAGSAAAGCCATCATGATCCAC			
THE TENEDOMEST SOT STITTOTSCACCIATORSAS			
TTA PRITTER TOT FOR AGT COT GACT GGTT			
othy, paking the trempara stail hit hat R	TATNIJAAN IBACOCANTNAN NUMEN AJ		
	TTATOT PRACTISTAS MARKOT SELLA MOL		

TERROR WATER TOTAL ACCACCATOACOMAT CATGAAGGTGTGGMATETER TOTAL EVALE TA 1 W STEETS FOR SAN MATTITATGICCATC TITCOTM.GCTCTACCCACTCCL FE ATTITUS THE TAKETATTETTE CAGCETTTATTOTEGAGAGCTTATGACCAATGTAAAAAA TWEEDA ACTAA BACTOMAAATOTTAGAAACCAGATACOCTOAAAGCAAGTCACAGTGAU ECUEUNA EGA IT - "MICATOTOTO TOTOTOTOTOGOCTOCOCCANTOCCTAGOTTOCCTOTOTOTAL FONE C GAAGROTGCASGCCCGGCCCCACCACAAGGTTTCATAGCCCTGTCTCAAGTGTT MATRITTTTCC ATCTTTTCAGCAAATCCTCTCATTTTTCTTGTGATGTCGGAAGAGTTCAGGGAAGGTTCAAGG GTGTATGGAAATGGATGATAACCAAAAAACCTCCAACTGTCTCAGAAGTCTCAGGAAACACCAGC TGGCAACTCAGAGGGTCTTCCTGACAAGGTTCCATCTCCAGAATCCCAGCATCCATACCAGAA AAAGAGAAACCCAGCTCTCCCTCTGGCAAAGGGAAAACTGAGAAGGCAGAGATTCCCATCC DE COLORA DEL AGRAGOA SENT EGGCATGA GAGGGA NACAGT COCTT CTGTACA DE SAGARANCA TA IMBUDI BAGAACAI BAAGAT CAAGA JAGAA JAGAA TAGAT GITAAAT**TAG**ATTI TAA TUIT DAAAA CARACAAACTGTGATTATTGTATTTACTTGTACTGCTGCTGCTTATCAATATTGCTCACCTTACAA ACTIGATATATTATTACCATTAGGAATTATAAAAATATTTCACAATCTACACTITCOAAATGTG CARTGTGGTAGGTAGAGAACCATGTTAGAAGTAATAATTGTTTCAGAATTAGAACTTGGCTTCC CAHACAATTTAAGTGTTGTGTAAAGATGTTGCTGTCAAAGTGATTAGACAGCCTGGCTATTCTG TCATTTGTTCACAGTGGTTTTACTGGGTACCCCCTAGGACCAGCCCTGTAGTGGACCGGCTGGA GCCTGCAGTAGAGGTTCTGTCAAAGCTGAGCCCCTTTAC CTTCAGTTTCACCCAGGACCTGCTA GTOCTAATTTTACCTACTAAATTGTATTTCACATAACCAAAGCTCAAAATCTACTTTCACTTGA GATTTTTAACACATTAATGATAAATTTTAATGCGTTC FT CATTTACTTAATAAGTGTTAATTTA CTTGATGAAAAGTCCGTATCATAATGTTCATGACTGAAGGTCAAA 3AAAAAGAAACAGCACCTT ATT CCAATTCTGGACTCATTTCAAG CCATGGCT GGTT CTGGCCAA STTTAAATAAA FICA GACT TALACTAAAGCCTGCTTCAGTGAACITTTTAAAGCTACCTGAATGAGTCTTCAGTTTCTAAGTC AAA

The following amino acid sequences <SEQ ID NOS. 2 and 3> are predicted amino acid sequences derived from the DNA sequence of SEQ ID NO. 1:

ATT IN MORE THE

MINANAPALEMBROCHUYGEAHLHEAGGYLPGESÇDWRT 1 IPALLVAVCLVGFVGNLCVIGILLH MANY HELEK HHELLILNLSLADLSLLLESAPIRATAYSKGVWOLGWFYCKGSDWFIHTCMAAKSLTIVVVAKVCFMYACEPA K. M. HHELYTIWSVLVAIWTVASLLPLPEWFFSTIPHHEGVEMCLVDVPAVAEEFMOMFGYLLYPLLAFGLPLF FASFYFWPAYTQCKKPGTKTQNLENQIRSKQVTVKLLSIAIISALLWLPEWVAWLWVWHLKAAGFAEFQGFI ALSQVLMFSISSANPLIFLUMSEEFREGLKGVWYWMHTKKPPTVSESQETPAGNSEGLEIFVYFDPEGFAGIP ENANTAME DER FYTEKAEIFILELVEÇFWHEFITUEGVQCHOFIFWEHEQZETGEGTY

## DOCKET NO: PHRM0020-100/00145.US1

HILL BAHLHBACKSYLBOLOODWRTIIP <b>allvavclvgfvgnlcvigillh</b> nawkgkboloheb <mark>lilnlsladl</mark>
LLLFSAPIRATATOKOTWOLGWFVCKSSDW <mark>FIHTCMAAKSLTIVVVAKVCFMY</mark> ASDFAR,TTHET <mark>YTIWSV</mark>
VAIWTVASLLPLPEWFFOTIPHHEGVEMOLVDVFAVAEEFMSMFGKLYPLLAFGLPLFFASFYFWFAYLOO
PP TOKTOMORNOTROKOVTVM <mark>llsiaiisallwlpewvawlwvw</mark> hlkaagfappo <mark>gfialsqvlmfsissa</mark>
PLIFLUMBEEFREGIKGVWKWMITKKPPTYSESQETFAGNSEGIPDKVPSPESPARIPEKEKEBREDDGKG
TEKARIPILEDVEÇFWHERDTVP3VQDNDPIPWEHEDQETGEGVK